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O1-NOV-1996 (TREMBLEGL 17, La
O1-JUN-2001 (TREMBLEGL 17, La
DISINTEGRIN-METALLOPROTEASE PI
 MEDILINE 96276398; PubMed-8694785;
Howard L., Lu X., Mitchell S., Griffths S., Glynn
Molecular cloning of MADM: a catalytically activ
Molecular cloning of MADM: a catalytically activ
disintegrin-metalloprotease
                                                                        SEQUENCE FROM N.A.,
TISSUE-BRAIN;
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
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Bos taurus (Bovine).
                                                                                                                       Bovidae; Bovinae; Bos.
NCBI_TaxID~9913;
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Pfam; PF01421; Reprolysin; 1.
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ZINC_PROTEASE; UNKN
se; Metalloprotease;
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N-LINKED (GLCNAC...) (POTENTIAL).
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Length

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Post-processing: Minimum Match 0%
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                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                               SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr:
13: sp_vertebr:
14: sp_unclass:
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Gapop 10.0 , Gapext 0.5
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1 MVLLRVLILLLSWAAGMGGQ......IQQPQRQRPRESYQMGHMRR 748
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sp_organel:*
sp_plant:*
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sp_unclassified:*
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sp_bacteria:*
SUMMARIES
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| 19     | 18                 | 17                 | 16                 | 15                 | 14                | 13                 | 12                 | 11                 | 10                | 9                  | 80                | 7                 | σ                 | 5                  | 4                  | ω                  | 2                 | _                  | NO.         | Result |
|--------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------|--------|
| 363    | 365.5              | 372.5              | 386                | 392.5              | 406               | 409.5              | 475                | 707                | 1345.5            | 1350.5             | 1450.5            | 1451              | 1452              | 2920               | 3333.5             | 3804.5             | 3852              | 3959               | Score       | )      |
| 8.9    | 8.9                | 9.1                | 9.4                | 9.6                | 9.9               | 10.0               | 11.6               | 17.3               | 32.9              | 33.0               | 35.5              | 35.5              | 35.5              | 71.4               | 81.5               | 93.0               | 94.2              | 96.8               | Match       | Query  |
| 610    | 873                | 914                | 819                | 845                | 75                | 600                | 686                | 162                | 1537              | 922                | 1239              | 1236              | 1238              | 544                | 691                | 749                | 748               | 748                | Length      | Query  |
| 13     | 13                 | 13                 | 4                  | 11                 | 6                 | 13                 | თ                  | 13                 | Ç,                | G                  | G                 | ഗ                 | v                 | 11                 | 4                  | 11                 | 6                 | 4                  | . DB        |        |
| Q9DGB9 | 042595             | 012960             | 013443             | Q61072             | 077633            | Q9PVK7             | Q94316             | 042568             | Q9VAI2            | 046354             | Q94902            | Q9NKF9            | 6MLA60            | Q10743             | Q10742             | 035598             | Q10741            | 014672             | 10          |        |
|        | 042595 xenopus lae | 012960 xenopus lae | Q13443 homo sapien | Q61072 mus musculu | 077633 sus scrofa | Q9pvk7 naja naja ( | Q94316 caenorhabdi | 042568 xenopus lae | Q9vai2 drosophila | O46354 caenorhabdi | Q94902 drosophila | Q9nkf9 drosophila | Q9vjw9 drosophila | Q10743 rattus norv | Q10742 homo sapien | O35598 mus musculu | Q10741 bos taurus | Ol4672 homo sapien | Description |        |

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1 MYLLRYLILLLSWAAGMGGQYGNPLNKYIRHYEGLSYNVDSLHQKHQRAKRAVSHEDQFL 60

96.8%; Score 3959; DB 4; Length 748; 96.9%; Pred. No. 0; ative 5; Mismatches 18; Indels 0;

0; Gaps

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Query Match 96.8 Best Local Similarity 96.9 Matches 725; Conservative

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| 01-JAN<br>01-JAN<br>01-JAN<br>01-JAN<br>01-JAN<br>ADAMII<br>ADAMII<br>HOMO:<br>EUKAII<br>MEDLII<br>ROSEUM<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MEDLII<br>MED | 25ULT<br>4672<br>014          | 20<br>21<br>22<br>22<br>23<br>23<br>24<br>25<br>26<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27   |
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| bl. 17, Last bl. 17, Last controller control   | 5,                            | 13   |
| 5, Last sequents, Last annotates; Craniatates; Catarrhii 9305925;  | ALIGNMENTS PRT; 748 Created)  | 09PT48<br>060411<br>042138<br>090495<br>09D495<br>09D491<br>090499<br>035674<br>09W6M5<br>092043<br>092043<br>092043<br>092043<br>09PZL5<br>090800<br>09PZL5<br>09VFR0<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09V120<br>09 |
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D 010743

C 010743;

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C 010743;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-UN-2001 (TrEMBLrel. 17, Last sequence update)

DE DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (M)

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Local Similarity
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PS00142;
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691 /
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ZINC_PROTEASE; UNKNOWN_1.
             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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Pred. No. 8.1e-265;
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PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00200; disintegrin; 1
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
SMART; SM00050; DISIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY.
-!- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.
EMBL; Z48444; CAA88359.1; -.
HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SPARGUE-DAWLEY TISSUE-BRAIN;
MEDLINE=96276398; PubMed=8694785;
HOWARD L. Mitchell S. Lu X. Griffiths S., Glynn
"Molecular cloning of MADM: a catalytically active
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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SEQUENCE FROM N.A.
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PSQGPCCTAQCAFKSKSEKCRDDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVCIN
           PSQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALCPASDPKPNFTDCNRHTQVCIN
                                                      EKKRNNCFVESGOPICGNGMVEOGEECDCGYSDQCKDECCFDANOPEGRKCKLKPGKQCS
                                                                                      DGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGIITVQNYGSHVPPKVSHITFAHE
                                                                                                                                              DGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGIITVQNYGSHVPPKVSHITFAHE
                                                                                                                                                                              GPELLRKKRINSAEKNTCQLYIQTDHLFFKYYGTREAVIAQISSHVKAIDTIYQTTDFSG
                                           EKKRNNCFVESGQPICGNGMVEQGEECDCGYSDQCKDECCFDANQPEGKKCKLKPGKQCS
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ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
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Pred. No. 4.
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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035598;
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01-JAN-1998
01-JAN-2001
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                                                                                                                                                                                                pfam; pF00200; disintegrin; 1.
pfam; pF01421; Reprolysin; 1.
SMARP; SM00050; DISIN; 1.
pROSITE; PS50215; ADAM_MEPRO; 1.
pROSITE; PS50214; DISINTEGRIN_2; 1.
pROSITE; PS50142; ZINC_PROTEASE; UNKNOWN,
SEQUENCE 749 AA; 83966 MW; 06CEC3EB2C
                                                                                                                                                                                                                                                                                  HSSP; P18619; 1FVL.
MEROPS; M.12.211; -.
MGD; MGI:109548; Adam10.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAM10 OR MKUZ.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97386452; PubMed-9244301;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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MEDLKDSSRLVVAHFMFEPAERYIKDRTLPFHSVIYHEDDINYPHKYGPQGGCADHSVFE
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                                                                                                                                               Score 3804.5;
Pred. No. 0;
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                        InterPro; IPR001762; Disintegri
InterPro; IPR001590; Reprolysin
InterPro; IPR000130; Zn_MTpeptd
Pfam; PF00200; disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
                                                                                                                                 SEQUENCE FROM N.A.

MEDLINB-96276398; PubMed-8694785;
Howard L., Lu X., Mitchell S., Griffths S., Glynn P.;
Howard L., Lu X., Mitchell S., Griffths S., Glynn P.;
"Molecular cloning of MADM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types."
Blochem. J. 317:45-50(1996).
                                                                                                                                                                                                                                                                        Q10742; Q92650;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DISINTEGRIN-METALLOPROTEASE MADM (FRAGMENT).
                                                                                                EMBL; 248579; CAA88463.1;
HSSP; P18619; 1FVL.
MEROPS; M12.210; -
                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                      010742
              PRINTS; PR00289; DISINTE SMART; SM00050; DISIN; 1
                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                   LKRRRPPQPIQQPPRQRPRESYQMGHMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGRFEGFIKTRGGTFYIEPAERYIKDRILPFHSVIYHEDDINYPHKYGPOGGCADHSVFE
                                                                                                                                                                                                                                                                                                                                                                                                                         LKRRRPPOPIOOPORORPRESYOMGHMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKMAPSTCASTGSLQWSKQFSGRTITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKMDPSTCASTGSVQWSRHFSGRTITLQPGSPCNDFRGYCDVFMFCRLVDADGPLARLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TALCPASDPKPNFTDCNRHTQVCINGQCAGSICEKYDLEECTCASSDGKDNKELCHVCCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TALCPASDPKPNFTDCNRHTQVCINGQCAGSICEKYGLEECTCASSDGKDDKELCHVCCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt KDDCCFDANQPEGKKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAKEGICNGF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDECCFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATSGDKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQPICGNGMVEQGEECDCGYSDQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATSGDKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQPICGNGMVEQGEECDCGYSDQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGIITVQNYGSHVPPKVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGNYIMYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGIITVQNYGSHVPPKVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGNYIMYA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLELNSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAVIAQISSHVKAIDTIYQTTDFSGIRNISFMVKRIRINTTSDEKDPTNPFRFPNIGVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAVIAQISSHVKAIDTIYQTTDFSGIRNISFMVKRIRINTTADEKDPTNPFRFPNIGVEK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMRKYQMTGVEEGARAHPEKHAASSGPELLRKKRTTLAERNTCQLYIQTDHLFFKYYGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RMRKYQMTGVEEVTQIPQEEHAA-NGPELLRKKRTNSAEKNTCQLYIQTDHLFFKYYGTR
   PS50215;
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                            (Human)
   ADAM_MEPRO;
                                                                                                                                                                                                                                     Chordata;
Primates;
                                                           Zn_MTpeptdse.
                                                                                   Disintegrin.
                                                                          Reprolysin
                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt M., Hoskins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blaze's R.G., Champe M., Pfelffer B.D.,
RA Bardon R.C., Rogers Y.H.C., Blaze's R.G., Champe M., Pfelffer B.D.,
RA Bardon R.C., Rogers Y.H.C., Blaze's R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Gherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebry J.M., Cavley S., Dahlke C., Davenport L.B., Dunkov B.C.,
Dunkov B.C., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Aliali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Mochect F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylrekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Syler E., Sjradling A.C., Stapleton M., Strong R., Smith T.,
RA Sylrekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Spier E., Sheng T., Zhong W., Zhong W., Zhou X., Smith H.O.,
Rhong X.H., Wang X.H., Wenter J.S., Zhoo Q., Zheng L.,
Rhong X.H., Wang X.H., Nalang G., Zhoo Q., Zheng L.,
Rhong S., Zhou X., Zhou X., Zhu X., Smith H.O.,
Rhong S., Sheng L., Sheng L.,
Rhong S., Sheng L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KUZ OR BG:DS07660.3 OR CG7147
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InterPro: IPR001390; Reprolysin.
InterPro: IPR001390; Reprolysin.
InterPro: IPR001390; Reprolysin.
InterPro: IPR001390; Reprolysin.
SMART; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM_MEPRO]; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS502142; ZINC_PROTEASE; UNKNOWN_1.
PROSITE; PS50142; ZINC_PROTEASE; UNKNOWN_1.
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 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNGTALCIRGECSGSPCLLWNMTKCFLTSTTLPHVSKRKLCDLACQDGNDTSTCRSTSEF
                                   NRHTQVCINGQCAGSICEKYGLEEC--TCASSDGKDDKELCHVCCMKKMDPSTCASTGSV
                                                                                                                                                KRDCFKASEGAFCGNKIVESGEECDCGFNEEECKDKCCYPRLISEYDQSLNSSAKGCTRR
                                                                                                                                                                                     RNNCFVESGQPICGNGMVEQGEECDCGYS-DQCKDECCF-----DANQPEGRKCKLK
                                                                                                                                                                                                                          PHDYPQECRPGGL-----NGNYIMFASATSGDRPNNSKFSPCSIRNISNVLDVLVGNT
                                                                                                                                                                                                                                                              PHDSGTECTPGESKNLGQKENGNYIMYARATSGDKLNNNKFSLCSIRNISQVLE----KK
                                                                                                                                                                                                                                                                                                   ASGGICEKYKTYTETVGGQYQSTKRSLNTGIITFVNYNSRVPPKVSQLTLAHEIGHNFGS
                                                                                                                                                                                                                                                                                                                      SSGGICEKSKLYSD------GKKKSLNTGIITVQNYGSHVPPKVSHITFAHEVGHNFGS
                                                                                                                                                                                                                                                                                                                                                                           CRNSYNGPHNAFCNEHMDVSNFLNLHSLEDHSDFCLAYVFTYRDFTGGTLGLAWVASASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASHGRDFHLRLKRDLNTFSNKLDFYDSKGPIDVSTDHIYEGEVIGDRNSYVFGSIHNGVF 135
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                                                                                                         PGKQCSPSQGPCCTA-QCAF--KSKSEKCRDDSDCAREGICNGFTALCPASDPKPNFTDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQLHKKSAPQQQQQPHPPKKYISGDEDFKYPHQKYTKEANFAEGAFYDPSTGRRLGSSAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ELLRKKRTNSA-----
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Pred. No. 3.5e-110;
11; Mismatches 263;
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AC Q9NKF9;
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence, DT 01-OCT-2000 (TrEMBLrel. 17, Last sequence, DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EKUZ PROTEIN.
GN KUZ OR BG:DS07660.3 OR G7147.
GN KUZ OR BG:DS07660.3 OR G7147.
CS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Pterygota; Drosophilidae; Drosophila.
                                                                                                                                                                                         RC STRAIN=Y, CN BW SP;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chaver C., Chew M., Clesiolka L., Doyle C.M.,
RA Butenhoff C., Champe M., Chaver C., Chew M., Clesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Siderin L.L., Rubin G.M.;
RA Sidmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE003407; AAP44800.1; -
DR FlyBase; FBgn001590; Reprolysin.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Reprolysin.
DR InterPro; IPR00130; Zn_MTpeptdse.
SMART; SM00050; DISIN 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS50214; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 1236 AA; 136343 MW; 40461AC17040C9AD CRC64;
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Matches 331
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the Drosophila melanogaster: the Adh region.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Y, CN BW SP;
MEDLINE=99403001; PubMed=10471707;
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                                                                                   LNKYIRHYEGLSYNVDSLHQKHQRAKRAVSHEDQFLRLDFHAHGRHFNLRMKRDTSLFSD
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Pred. No. 4.2e
24; Mismatches
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KUZ OR BG:DS07660.3 OR CG7147
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 melanogaster (Fruit fly).
                                              (TrEMBLrel.)
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"KUZ, a conserved metalloprotease-disintegrin in Drosophila neurogenesis.";
Science 273:1227-1231(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurogenesis
SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0015954; kuz
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            DSGTECTPGESKNLGQKENGNYIMYARATSGDKLNNNKFSLCSIRNISQVLE----KKRN
                                                                                                  NSYNGPHNAFCNEHMDVSNFLNLHSLEDHSDFCLAYVFTYRDFTGGTLGLAWVASASGAS
                                                                                                                                                     RGRKYEVDEKTREEITSLIAHHVTAVNYIYRNTKFDGRTEHRNIRFEVQRIKIDDDSACR
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DYPQECRPGGL---
                                                                           GGICEKSKLYSD---
                                                                                                                                                                                                                                                          LHKKSAPQQQQPHPPKKYISGDEDFKYPHQKYTKEANFAEGAFYDPSTGRRLGSSANVA
                                                                                                                                                                                                                                                                                                                                       SVIY---HEDDINYPHKYGPQGGCA-DHSVFERMRKYQMTGVEEVTQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                             LMEDLKDSSRLVVAH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAHGRHFNLRMKRDTSLFSDEFKVETSNKVLDYDTSHIYTGHIYGEE-----GSLAMGLL
                                                GGICEKYKTYTETVGGQYQSTKRSLNTGIITFVNYNSRVPPKVSQLTLAHEIGHNFGSPH
                                                                                                                   -DEKDPTNPFRFPNIGVEKFLELNSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSS
                                                                                                                                                                                                         DWHQLVHERVRRATDNGAGDRGSSGGSGRGREDNKNTCSLYIQTDPLIWRHIREGIADHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1239 AA;
                                                                                                                                                                             ---GTREAVIAQISSHVKAIDTIYQTTDFSG---IRNISFMVKRIRINTTA---
                                                                                                                                                                                                                                   ELLRKKRTNSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.0%;
                                                               -GKKKSLNTGIITVQNYGSHVPPKVSHITFAHEVGHNFGSPH
NGNYIMFASATSGDRPNNSKFSPCSIRNISNVLDVLVGNTKR
                                                                                                                                                                                                                                                                                                                                                                                          ------TLPFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134;
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Pred. No. 4.6e-1
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                                                                                                                                                                                                                                   -EKNTCQLYIQTDHLFFKYY------
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Best Local
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046354;
01-JUN-1998
01-JUN-1998
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PROSITE; PS50214; DISINTEGRIN_2; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

SEQUENCE 922 AA; 101572 MW; BAE4E5E65875CDB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001330; Zn_MTPeptdse.
SMART; SM00050; DISIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF024614; AAB97161.1; -. EMBL; Z96047; CAB09416.1; -. HSSP; P18619; LFVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98088688; PubMed=9428412;
Wen C., Metzstein M.M., Greenwald I.;
"SUP-17, a Caenorhabditis elegans ADAM protein related
KUZBANIAN, and its role in LIN-12/NOTCH signalling.";
Development 124:4759-4767(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans,
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
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                                                NGLNNFIDNFETLNYRATHVANQVTRRKRSIDSAASHYQEPIGFRFNAYNRTFHVQLHPI
                                                                                              NPLNKYIRHYEGLSYNVDSLHQKHQRAKR----AVSHEDQFLRLDFHAHGRHFNLRMKR-
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36.9%;
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Caenorhabditis.
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Last annotation updat
                                                                                                                                                                      Score 1350.5; DB 5
Pred. No. 4.9e-102;
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O1 MAY-2000 (TrE
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CG1964 PROTEIN.
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  STRAIN-BERKELEY;
MEDLINB-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle
George R.A., Lewis S.E., Richards S., Ashburner M., Henderso
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLQTCDGRNAQCPVSPPKHDGIPCQDSTKVCSSGQCNGSVCAMFGLEDCFL-
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(TrEMBLrel. 17,
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           M., Henderson
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A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry D.M., Melson D.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Wooldage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RC - Inmiarity: To NEUTRAL ZINC METALLOPEPTIDASES, ZINC-BINDING REGION

CC - Inmiarity: To NEUTRAL ZINC METALLOPEPTIDASES, ZINC-BINDING REGION
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Babril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M., H., Ibewann C.,
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HSSP; P18619; 1FVL.
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                                                                                  SDVNMQKQQFTGGGLNSATPAKTHCASEKLRKKRWLPEELAMSDAPAPTYNRNPPLPLDL 248
                                                                                                                                                                     DDINYPHKYGPQGG-----
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                                                                                                                                                                                                                                                                                                                                     HIYTGHIYGEEGSLAMGLLLMEDLKDSS-RLVVAHFMFEPAERYIKD-RTLPFHSVIYHE 158
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PS50214; DISINTEGRIN_2;
PS00142; ZINC_PROTEASE;
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Pred. No. 2.5
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01-JAN-1998
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                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopudinae; Xenopus.
                                                                                                              SEQUENCE FROM N.A. MEDLINE-97386452; PubMed-9244301;
                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                 KUZBANIAN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               042568;
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"Kuzbanian controls proteolytic processing of Notch and mediates lateral inhibition during Drosophila and vertebrate neurogenesis Cell 90:271-280(1997).
                                                                                                                                                                                                       NCBI_TaxID-8355;
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R SMART; SM00050; DISIN; 1.
R PROSITE; PS50214; DISINTEGRIN_2; 1.
NON_TER 162 162
SEQUENCE 162 AA.
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Best Local
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Q94316;
Q1-FEB-1997
                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mamurray A., Mortimore B., O'Callaghan M
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of
                           Submitted (SEP-1996) to t
EMBL; U70844; AAB09097.1;
HSSP; P17494; 1KST.
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                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                             eLegans
                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY TO METALLOPROTEASES.
                                                                     Waterston
                                                                                                                           Submitted
                                                                                                                                                                                              Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID~6239;
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                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 YSDOCKDECCFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAREG
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  IPR001590;
                                                                                                                           (OCT-1996)
              IPR001762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematoda; Chromadorea;
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72.2%;
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Reprolysin
              Disintegrin.
                                                     the EMBL/GenBank/DDBJ databases
                                                                                                                          the EMBL/GenBank/DDBJ databases
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Last annotation updat
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Pred. No. 2
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1.7e-50;
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Best Local Similarity
Matches 179; Conserv
09PVK7
09PVK7;
01-AAY-2000
01-MAY-2000
01-JUN-2001
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SMART; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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               (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
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InterPro; IPR001870; Pep_M12B_propep
InterPro; IPR001890; Reprolysin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF00200; disintegrin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
PFNNTS; PR00289; DISINTEGRIN.
ProDom; PD000664; DISINTEGRIN.
PRODOM; PD000664; DISINTEGRIN; 1.
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SIGNAL
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PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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HSSP; P17494; 1KST.
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Submitted (MAY-1998) to the
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroldea;
Elapidae; Elapinae; Naja.
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                                                                            HEAQCDSEE----CCEKCKFKGAGAECRAAKDDCDLPELCTGQSAECPTDVFQRNGLPC-Q
                                                                                                                                                                                                                                       KKRNNCFYES-----GQPICGNGMYEQGEECDCGYSDQCKDECCFDANQPEGRKCKLK
                                                                                                                                                                                                                                                                                                                             GHNLGMNHDKGF-CTCGENK-----CVMSTRRTK----PAYQFSSCSVREHQRYLL
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                                                                                                                                                                                                       RDRPQCILNKPLSTDIVSPPICGNYFVEVGEECDCGSPADCQSACC---
                                                                                                                                                                                                                                                                                                                                                                                      GHNFGSPHDSGTECTPGESKNLGQKENGNYIMYARATSGDKLNNNKFSLCSIRNISQVLE
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horst R., Vogel C.-W.;
998) to the EMBL/GenBank/DDBJ
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Best Local
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Q61072; Q60618; Q61853;
Q61072; Q60618; Q61853;
Q1-JUL-1997 (TrEMBLrel 04, Cr.
Q1-JUL-1997 (TrEMBLrel 17, La.
CELLULAR DISINTEGRIN RELATED P.
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                                                                 "MDC9, a widely expressed
SH3 ligand domains.";
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DISINTEGRIN-METALLOPROTEINASE PRECURSOR (FRAGMENT).
SEQUENCE OF 426-575 FROM N.A
                                                                                                         MEDLINE=96178079; PubMed=8647900;
Weskamp G., Kraetzschmar J.R., Re
                                                                                                                                                                                                                         NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                               ADAM9 OR MLING OR MDC9.
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                                                                                                                                                                            SEQUENCE FROM N.A.
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Expression of articular cartilage metalloproteinases by chondrocytes
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bmltted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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>S50215; ADAM_MEPRO; 1.
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                                                                                    J.R., Reid
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D PROTEIN PRECURSOR (MELTRIN GAMMA).
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Pred. No. 4.6e-26;
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Sciurognathi; Muridae;
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DOMAIN
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PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPR000561; EGF-like.
InterPro; IPR000570; Pep-M12B_prop
InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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1: FUNCTION: MAY MEDIATE CELL-CELL OR CELL-MATRIX INTERACTIONS.
1: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
1: TISSUE SPECIFICITY: WIDELY EXPRESSED.
1: SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A metalloprotease-disintegrin participating in myoblast fusion.";
Nature 377:652-656(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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MGD; MGI:105376; Adam9
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Proc. Natl. Acad. Sci. U.S.A. !
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                                                                                                                 LRLRWLLACGLLGPVLEAGRPDLEQTVHLS--SYEIITPWRLTRERREALGPSSQQISYV
                                      IQAQGKQHIIHLERNTDLLPNDFVVYTYDKEGSLLSDHPNVQSHCHYRGYVEGVQNSAVA
                                                                        FHAHGRHFNLRMKRDTSLFSDEFKVETSNK----VLDYDT--SHI-YTGHIYGEEGSLA- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U06145; AAA18424.1; -. U41765; AAC52446.1; -. D50412; BAA08913.1; -.
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SM00181; EGF; 1
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MGLLLMEDLKDSSRLVVAHFMFEPAERYIKDRTLPFHSVIYHEDDINYPHKYG
                                                                                                                                                                                               Conservative
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25.3%;
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U.S.A. 91:2748-2751(1994).
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                                        463 DCQFLPGGSMCRGKTSECDVPEYCNGSSQFCPPDVFIQNGYPCQNSKAYCYNG----MC 517
                                                     514 QCAFKSKSEKCR-DDSDCAREGICNGFTALCPASDPKPNFTDCNRHTQVCINGQCAGSIC 572
                                                                                 288 NPFREPNIGVEKFLE-----LNSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGG 342
                                                                                                                                                                                                                                                         173 LRCGVSNRDT-----EKEGTQGDEEEH-PSVTQLLRRRRAVLPQTRYVELFIVV 220
                                                                                                                                                                                                                                                                                                                 130 VSACFGLRGLLHLEN------ASFGIEPLH-----NSSHFEHIFYPMDGI---HQEP 172
                                                                                                                                                                                                                 272 NIIGGAGDVLGNFVQWREKFLITRRRHDS---AQLVLKKGF-GGTAGMAFVGT----- 320
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Search completed: April 1, 2002, 15:12:06 Job time: 688 sec

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Run on:
                                                                                                  OM protein - protein search, using sw model
          April 1, 2002, 15:12:06; Search time 98.78 Seconds (without alignments)
392.409 Million cell upo
                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
cell updates/sec
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Total number of hits satisfying chosen parameters: 473505

473505 seqs, 146272329 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL\_17:\*
1: sp\_archea:\*
2: sp\_bacteria sp\_archea:\*
sp\_bacteria:\*

sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_organelle:\*
sp\_phage:\* sp\_fungi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 19                 | 18                 | 17                 | 16                 | 15                 | 14                 | 13                 | 12                 | 11                | 10                 | 9      | 8                 | 7      | ο,                | ъ                 | 4.                 | ω                  | ν                  | ш.                 | Result                |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|-------------------|--------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-----------------------|
| 289.5              | 290                | 291.5              | 292.5              | 293                | 298.5              | 366                | 390                | 406               | 683                | 737    | 737               | 737    | 754               | 1449              | 1463               | 1466               | 1472               | 1472               | Score                 |
| 19.5               | 19.5               | 19.6               | 19.7               | 19.7               | 20.1               | 24.7               | 26.3               | 27.4              | 46.0               | 49.7   | 49.7              | 49.7   | 50.8              | 97.6              | 98.6               | 98.8               | 99.2               | 99.2               | Query<br>Match        |
| 609                | 728                | 845                | 610                | 620                | 600                | 686                | 162                | 75                | 922                | 1239   | 1238              | 1236   | 1537              | 748               | 749                | 544                | 748                | 691                | Query<br>Match Length |
| 13                 | 4                  | 11                 | 13                 | 13                 | 13                 | S                  | 13                 | თ                 | υı                 | 5      | ر.                | G      | υı                | 6                 | 11                 | 11                 | 4                  | 4                  | DB                    |
| Q90282             | Q9BZ11             | Q61072             | Q9DGB9             | 042138             | Q9PVK7             | Q94316             | 042568             | 077633            | 046354             | 094902 | 6MCA60            | Q9NKF9 | Q9VAI2            | Q10741            | 035598             | Q10743             | 014672             | Q10742             | ΙĐ                    |
| Q90282 crotalus at | Q9bz11 homo sapien | Q61072 mus musculu | Q9dgb9 crotalus at | O42138 agkistrodon | Q9pvk7 naja naja ( | Q94316 caenorhabdi | 042568 xenopus lae | 077633 sus scrofa | O46354 caenorhabdi |        | Q9vjw9 drosophila |        | Q9vai2 drosophila | Q10741 bos taurus | O35598 mus musculu | Q10743 rattus norv | 014672 homo sapien | Q10742 homo sapien | Description           |

| ť               | ъ.          | 44     | 43                 | 42                 | 41     | 40     | 39                 | 38                 | <b>37</b> | 36     | 35     | 34                 | ω             | 32                 | 31     | 30     | 29                 | 28     | 27                 | 26                 | 25     | 24     | 23                 | 22                 | 21      | 20                 |
|-----------------|-------------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|-----------|--------|--------|--------------------|---------------|--------------------|--------|--------|--------------------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|---------|--------------------|
|                 | יונ<br>פוני | 253    | 254                | 257                | 257    | 257    | 259                | 261                | 262       | 267    | 267.5  | 267.5              | 267.5         | 268                | 269.5  | 269.5  | 270                | 273    | 277.5              | 279                | 280    | 280    | 280.5              | 282                | 282.5   | 286.5              |
| F               | 11.         | 17.0   | 17.1               | 17.3               | 17.3   | 17.3   | 17.5               | 17.6               | 17.7      | 18.0   | 18.0   | 18.0               | 18.0          | 18.1               |        | 18.2   | 18.2               | 18.4   | 18.7               | 18.8               | 18.9   | 18.9   | 18.9               | 19.0               | 19.0    | 19.3               |
| 0.74            | 0 0         | 583    | 903                | 789                | 617    | 505    | <b>4</b> 51        | 788                | 761       | 1569   | 918    | 918                | 857           | 419                | 873    | 697    | 735                | 616    | 604                | 606                | 610    | 609    | 920                | 610                | 914     | 819                |
| ı               | n (         | ú      | 1                  | 11                 | 13     | 13     | 13                 | 11                 | 11        | ഗ      | 4      | 4                  | 4             | 13                 | 13     | 11     | 11                 | 13     | 13                 | 13                 | 13     | 13     | 11                 | 13                 | 13      | 4                  |
| 73671J          | 2000        | 09VXL1 | Q61824             | Q63180             | Q90499 | 073795 | Q9PT49             | 035227             | Q9R160    | Q9VFHO | Q9BZL5 | Q9н013             | Q9UHP2        | Q92043             | 042595 | Q9R158 | Q60411             | Q90495 | Q9PT48             | Q98UF9             | 093523 | Q9W6M5 | 035674             | Q9YI20             | 012960. | Q13443             |
| Asia osom crafe |             | Д.     | Q61824 mus musculu | Q63180 rattus norv |        |        | Q9pt49 atractaspis | O35227 mus musculu | $\sim$    | dros   | homo   | Q9h013 homo sapien | $\overline{}$ | Q92043 crotalus at | -      | _      | Q60411 cavia porce |        | Q9pt48 atractaspis | Q98uf9 bothrops ja | -      |        | 035674 mus musculu | Q9yi20 agkistrodon | 0       | Q13443 homo sapien |

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Tidentification and characterization of a pro
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Best Local Similarity
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MEDLINE-97450992: PubMed-9305925;

Rosendahl M.S., Ko S.C., Long D.L., Brewer M.T., Rose Rosendahl E., Anderson L., Pyle S.M., Moreland J., Meyers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                Score 1472; DB 4;
Pred. No. 2e-131;
0; Mismatches 0,
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Kohno T.,
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1 NSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGII

Query Match Best Local S Matches 260

Similarity

98.8**%**; 99.2**%**;

Score 1466; DB 11; Pred. No. 5.1e-131; 2; Mismatches 0;

Length Indels

544;

Gaps II 60

0

Conservative

| CARBOHYD 347 347 N-LINKED (GLCNAC) (POTENTIAL). SEQUENCE 544 AA; 60444 MW; F75E0E8D6C88A7DD CRC64;   | SOFI   |
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| 235 235 N-LINKED (GLCNAC) (POTENTIAL   |        |
| 74 74 N-LINKED (GLCNAC) (POTENTIAL   |        |
| 63 63 N-LINKED (GLCNAC) (POTENTIAL   |        |
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| Hydrolase; Metalloprote  |        |
| PS00142; ZINC_PROTEASE;  |        |
| PROSITE; PS50214; DISINTEGRIN_2; 1.  |        |
| PS50215;   |        |
| )0050; p   |        |
| 9; DISINTEGE   |        |
| 421; Reprol  |        |
| )200; disintegrin  |        |
| IPR000130;   |        |
| IPR001590; Reprolysin.   |        |
| nterPro; IPR001762; Disintegrin.   |        |
| MEROPS: M12.210:   |        |
| HSSP; P18619; 1FVL.  |        |
| L: Z48444: CAA88359.1;   |        |
| - SIMILARITY: HIGH IN THE MIDDLE REGION TO DISTUTEGRING  | 38     |
| METALLOPROTEASE). ALSO KNOWN A   |        |
| -I- GUNCELLULAR ECCAILON: INTEGRAL MEMBRANE FROTEIN<br>-I- GIMTIADITY BETONGS TO DEPOTIDAGE FAMILY WIDE 771NO  |        |
| 10Chem. J. 31/:45-50(1996).  |        |
| isintegrin-metalloprotease expressed in various cell types.";  |        |
| malian   | RT     |
| oward L., Mitchell S., Lu X., Griffiths S., Glynn P.,  |        |
| MEDLINE-96276398; PubMed-8694785;  |        |
| TRAIN-SPRAGUE DAWLEY: TISSUE-BRAIN:  |        |
| EDITENCE FROM N A  |        |
| NCBL_TGXIU=IUIIO;  | Z Z    |
| dentia; Sciurogna  |        |
| a; Chordata; Craniata; Vertebrata; E   |        |
| Rat).  | 20     |
| FRAGMENT).   |        |
| METALLOPROTEASE PREC   |        |
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| ATTEMPT TO 1 OT CTO  |        |
| 210743 PRELIMINARY; PRT; 544 AA.   |        |
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| ω  | RESULT |
| 544 PASDPKPNFTDCNRHTQVCING 565   | В      |
| 241 PASDPKPNFTDCNRHTQVCING 262   | Qγ     |
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| 484 CFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALC 543   | Db     |
| LOI CFUANQPEGRACKLAFGXQCSFOQGSCCTAQCAFKSXSEXCADDSDCAREGICNGFTALC 240   | QΥ     |
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Best Local (
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SMART; SM00050; DISIN; 1.
PROSITE; PS02115; ADAM_MEPRO; 1.
PROSITE; PS02145; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 749 AA; 83966 MW; 06CEC3EB2C5F4F94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            "Kuzbanian controls proteolytic processing of Notch lateral inhibition during Drosophila and vertebrate Cell 90:271-280(1997).
EMBL, AFO11379; AAC53303.1; -.
HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan D., Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97386452; PubMed=9244301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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               CFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAREGICNGFTALC
                                       GDKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQPICGNGMVEQGEECDCGYSDQCKDDC
                                                    GDKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQPICGNGMVEQGEECDCGYSDQCKDEC
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                                                                                                                                         NSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGII
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pro; IPR001590; Reprolysin.
pro; IPR000130; Zn_MTpeptdse.
pF00200; disintegrin; 1.
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Rodentia;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                      Score 1463; DB 11;
Pred. No. 1.4e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        749
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                                                                                                                                                                                                                   Length
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neurogenesis.";
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1 NSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGII

Query Match Best Local : Matches

Local Similarity

97.68; 97.78;

Conservative

4;

Mismatches

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Gaps 60

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Length Indels

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Q10741;
01-NOV-1996
                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                               CHAIN
CHAIN
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                                                                                                                                                                                                          METAL
METAL
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Pfam; PF01421; Reprolysin; 1.
SMART; SM00050; DISIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disintegrin-metalloprotease expressed in various cell types."; Biochem. J. 317:45-50(1996),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seque
01-JUN-2001 (TrEMBLrel. 17, Last annot
DISINTEGRIN-METALLOPROTEASE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METALLOPROTEASE).
-!- SIMILARITY: HIGH, IN THE MIDDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12C (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN. LEVELS IN KIDNEY, SPLEEN, LUNG AND HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METALLOPROTEINASE) (MADM).
                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; M12.210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z21961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96276398; PubMed=8694785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Integrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Howard L., Lu X., Mitchell S., Griffths S., Glynn P.;
Molecular cloning of MADM: a catalytically active mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISINTEGRIN_2; 1.
ZINC_PROTEASE; UNKNOWN_1.
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213
455
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                                                                                             CYTOPLASMIC (POTENTIAL).

BY SIMILARITY (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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Last annotation update)
PRECURSOR (EC 3.4.24.-)
Score 1449; Db v,
                                                                                                                                                                                                                                                                                                                                                                 DISINTEGRIN
                                                                                                                                                                                                                                                                                                                                                                                     METALLOPROTEINASE
                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Zinc; Signal;
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RX MEDLING-20196006; pubMed-10731132;
RX MEDLING-20196006; pubMed-10731132;
RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA Ballew R.M., Dayle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Hander R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hallew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Beson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Bottler R., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottler R., Chandra I.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hortis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Mixon K., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Haller B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Stapleton M., Strong R., Sun E.,
RA Haller B.C., Moshrefi A., Rodder
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Pterygota; Neoptera; F
Ephydroidea; Drosophij
NCBI_TaxID=7227;
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Q9VAI2;
01-MAY-2000 (TrE
01-MAY-2000 (TrE
01-JUN-2001 (TrE
CG1964 PROTEIN.
CG1964.
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Last sequence update)
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Best Local S
Matches 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flybase; FBgn0039688; CG1964.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
pfam; PF01421; Reprolysin; 1.
SMARR; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM_MEPRO; 2.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc.
SEQUENCE 1537 AA; 168796 MW; 46A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NKF9;
01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                SEQUENCE FROM N.A.

STRAIN=Y, CN BW SP;

MEDLINE=99403001; PubMed=10471707;

Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis Doyle C., Galle R., George R., Harris N., Hartzell G., Harrey Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshre Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whit Celniker S., Rubin G.M.;

"An exploration of the sequence of a 2.9-Mb region of the geno
                                                  Genetics [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003770; AAF56926.1; HSSP; P18619; 1FVL.
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-!- SIMILARITY: TO NEUTRAL ZINC METALLOPEPTIDASES,
                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9NKF9
                                                                                                        Drosophila melanogaster:
                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVPQCPPSVNKPNKTICNKEF-VCYMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCCFPMSRQPRLDETPCTLTPHARCSPSQGPCCTTDCKLKF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKKNNNKFSTCSLKSIEPVLNAKARSMKGCFTEPQSSICGNGVVEPGEQCDCGWEEDCKD
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145; Conser
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, CN BW
                                                                          153:179-219(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
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                                                                                                        Adh
                                                                                                     region.";
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                                                                                                                                                                                                        G., Harvey D.,
C., Moshrefi A.,
                                                                                                                                                                                                                                                           Davis
                                                                                                                                                                                  Whitelaw
                                                                                                                                genome
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Best Local
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KUZ OR BG:DS07660.3 OR CG7147.

KUZ OR BG:DS07660.3 OR CG7147.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Musco

Therygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMO050; DISIN; 1.

PROSITE; PS50215; ADAM_MEDRO; 1.

PROSITE; PS50214; DISINTEGRIN_2;

PROSITE; PS00142; ZINC_PROTEASE;

PROSITE; PS00142; AA; 136343 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VJW9;
                                 MEDLINE-2019606; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.E.,
Escape R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0015954; kuz.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                            STRAIN-BERKELEY;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
 Ballew R.M.,
Beeson K.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOKCKEETECSWSSTCNGTTAECPEPRHRDDKTMCNNGTALCIRG
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Basu A., Baxendale J., Bayraktaroglu L., Beasley Benos P.V., Berman B.P., Bhandari D., Bolshakov (
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50.2%;
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40461AC17040C9AD CRC64;
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RESULT Q94902

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Q94902; Q94902; 01-FEB-1997 01-FEB-1997

(TrEMBLrel. 02, (TrEMBLrel. 02,

Last sequence update)

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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liuk K., Mattei B., McIntosh T.C., McLeod M.P., Liu Y., Li Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA McRillov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA McRillov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA McIntosh D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skipski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skipski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skipski M.P., Smith T.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Wooddage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Yeb J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,

RA Zheng C.B., Wyers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster.";

BCMBL, RABO3640; AAF3318-1; -.

DR EMBL, BEO3640; AAF3318-1; -.
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Best Local :
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Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
Generry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmai
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Honston V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN_;
PROSITE: PS00142; ZINC_PROTEASE;
SEQUENCE 1238 AA; 136407 MW;
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751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLNTGIITVQNYGSHVPPKVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGNYI 113
HOKCKEETECSWSSTCNGTTAECPEPRHRDDKTMCNNGTALCIRG
                                                                                                                                                                                                                            CGYS-DQCKDECCF-----DANQPEGRKCKLKPGKQCSPSQGPCCTA-QCAF--KSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSLEDHSDFCLAYVFTYRDFTGGTLGLAWVASASGASGGICEKYKTYTETVGGQYQSTKR 577
                                                                    SEKCRDDSDCAREGICNGFTALCPASDPKPNFTDCNRHTQVCING
                                                                                                                                                    CGFNEEECKDKCCYPRLISEYDQSLNSSAKGCTRRAKTQCSPSQGPCCLSNSCTFVPTSY
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50.28;
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96D924B6188AC472 CRC64;
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Best Local S
Matches 143
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR00130; Zn_MTpeptdse.
SMART; SM0050; DISIN; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS500142; ZINC_PROTEASE; UN
                                                                                                                                 046354;
046354;
01-JUN-1998
01-JUN-1998
01-JUN-2001
SEQUENCE FROM N.A.
MSQLINE=98088688; PubMed=9428412;
Wen C., Metzstein M.M., Greenwald
"SUP-17, a Caenorhabditis elegans
                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat,
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                            SUP-17
                                                                                                                       ADAM 10.
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Rooke J., Pan D., Xu T., Rubin G.M.;
"KUZ, a conserved metalloprotease-disintegrin
in Drosophila neurogenesis.";
Science 273:1227-1231(1996).
EMBL; U60591; AAC47275.1; -.
EMBL; U60591; AAC47275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                        CGFNEEECKDKCCYPRLISEYDQSLNSSAKGCTRRAKTQCSPSQGPCCLSNSCTFVPTSY
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                                                                                                                                                        (TrEMBLrel.
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                                                                                  Nematoda;
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                                                                     oda; Chromadorea;
Caenorhabditis.
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Last sequence up
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Pred. No. 2e-61;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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 ADAM
protein
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                                                                                                                                            update)
                                                                                  Rhabditida; Rhabditoidea;
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6
Drosophila
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Best I
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01-NOV-1998
01-NOV-1998
01-JUN-2001
           Integrin.
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NON_TER
                                                                                    Flannery C.R., Little C.B., Caterson B., Hughes C.E.; "Expression of articular cartilage metalloproteinases by che in fresh tissue and explant, monolayer and agarose cultures Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF069645; AAC23529.1; -.
                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) DISINTEGRIN-METALLOPROTEINASE PRECURSOR (FRAGMENT).
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 SEQUENCE
                                                 PROSITE;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                        Eukaryota;
Mammalia; 1
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InterPro;
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EMBL;
HSSP;
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                                                                                                                                                                           NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development 124:4759-4767(1997)
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rPro; IPR000130; Zn_MTpeptdse.
T; SM00050; D1SIN; 1.
ITE; PS50215; ADAM_MEPRO; 1.
ITE; PS50214; DISINTEGRIN_2; 1.
ITE; PS50214; DISINTEGRIN_2; 1.
ITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
ENCE 922 AA; 101572 MW; BAE4E5E6587
                                                                                                                                                                                                                                                                                                                                                                   PDTCSLHGKNEEKICRQESECSNLQTCDGRNAQCPVSPPKHDGIPCQDSTKVCSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPS-GSSGGICEKSKLYSDGKK----KSL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASATSGDKPNNGKFSPCSVKNISAVLAVVLKSMPVDPTRNASPVGIGKRNCFQERTSAFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARATSGDKLNNNKFSLCSIRNISQVL-----EKKRN-----NCFVESGQPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTGIVTLVNYGNRVPARVSQLTLAHEIGHNFGSPHDFPAECQPG-----LPDGNFIMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTGIITVQNYGSHVPPKVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGNYIMY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSQRNHSAFCLAYALTFRDFVGGTLGLAWVASPQFNTAGGICQVHQRYNEGSRGWVYRSL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF024614; AAB97161.;
Z96047; CAB09416.1;
P18619; IFVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                 PS50215;
                                                                                                                                                                                        Eutheria;
                                                               IPR001590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001762; Disintegrin.
75
                                                                                                                                                                                                                 (Pig).
                                                                                                                                                                                                                                                   (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
AA;
                                                 ADAM_MEPRO;
8224 MW;
                                               ; Reprolysin.
האת MEPRO; 1.
                                                                                                                                                                                     Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.0%;
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17,
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                                                                                                                                                                                                                                                                              Created)
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С03B70С901333557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 683;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAE4E5E65875CDB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                      75
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CRC64;
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                                                                                                                                                                                                   Euteleostomi;
                                                                                                             chondrocytes
res.";
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RESULT 0425061
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1D 268
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Q94316
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SCCORETTIAN
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Best Local
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                                                                                                                                                                                                                              Q94316;
Q94316;
  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILARITY TO METALLOPROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan D., Rubin G.M.;
"Kuzbanian controls proteolytic processing of Notch lateral inhibition during Drosophila and vertebrate Cell 90:271-280(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel 05, 01-JAN-1998 (TrEMBLrel 05, 01-JUN-2001 (TrEMBLrel 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001762; Disintegrin.
PRINTS; PR00289; DISINTEGRIN.
SMART; SM00050; DISIN; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF011380; AAC60248.1; -. HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97386452; PubMed-9244301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; M12.210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KUZBANIAN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  042568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 YSDQCKDECCFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAREG 231
                                                                                                                                                                                                                                                                                                                                                                                                                             232 ICNGFTALCPASDPKPNFTDCNRHTQVCING 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 FVESGQPICGNGMVE 163
                                                                                                                                                                                                                                                                                                                                                                               61 TCNGNSAQCPPSEPRENLTECNRATQVCIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSDQCKDECCYDANQPENLKCTLKPGKQCSPSQGPCCTTGCTFKRAGENCREESDCAKMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHDSGTECTPGESKNLGQKENGNYIMYARATSGDKLNNNKFSLCSTRNISQVLEKKRNNC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162
17780 MW; E2E0BE1670494492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.3%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 390; DB 13,
Pred. No. 1.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 2.3e-31;
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  91
                                                                                                                                                                                                                                                    989
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                                                                                                                                                                                                                                                    Å
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neurogenesis.";
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                                                                                                                RESULT
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Best Local (
Q9PVK7 PRELII
Q9PVK7;
01-MAY-2000 (Trem
01-MAY-2000 (Trem
01-JUN-2001 (Trem
COBRIN PRECURSOR.
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SMART; SM00050; DISIN; 1.
PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Morthnore B., O'Callaghan M.,
Parsons J., Percy C., Hikken L., Roopra A., Saunders D., Shownkeen J
smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001762; Disintegrin, InterPro; IPR001590; Reprolysin. InterPro; IPR000130; Zn_MTpeptdse.
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Connell M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE~94150718; PubMed=7906398;
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SEQUENCE FROM N.A.
                                                                                                                                                               518
                                                                                                                                                                                                                               465
                                                                                                                                                                                                                                                                                           405
                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                          231 GICNGFTALCPASDPKPNFTDCNRHTQVCINGVSI 265
                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                                    292 DFCLVHLVTARTFREVATLGLAYVSYKKWDETAGGICSKQETF-NGRVAYINVLLSTSFA
                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 DYCLAYVFTDRDFDD-GVLGLAWVGAP--SGSSGGICEKSKLYSDGKKKSLNTGIIT--V 62
                                                                                                                                                             AVCNGFSGECPSAPPVRDGQECLEGGE-CLNGVCL
                                                                                                                                                                                                                                                                                                                                                      NSEQSTYPLITKEIDIVVSHEYGHAWGATHDPTIDSDDPDVEECSPND-----QNGGKY 404
                                                                                                                                                                                                                                                         SDOCKDECCFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKC--RDDSDCARE
                                                                                                                                                                                                                                                                                                                      IMYARATSGDKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQPICGNGMVEQGEECDCGY
                                                                                                                                                                                                                                                                                                                                                                                  QNYGSHVP--PKVSHITFAHEVGHNFGSPHD-----SGTECTPGESKNLGQKENGNY 112
                                                                                                                                                                                                                                                                                        LMSQYAQKGYDANNVLFSPCSRKLIRDVLIGKWESCFQEEMTSFCGNGIVEDGEECDNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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               (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.7%;
33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77298 MW;
                                                                                                                                                                                                                           -DKFCRLAVGAKCSPLNHICCTPTCQFHNSTHVCLPGDSLLCKAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
               Last sequence update)
Last annotation update)
                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 366; DB 5;
Pred. No. 1.7e-26;
0; Mismatches 112;
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66D58008A207AE49 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                      464
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RESULT
O42138
ID
O42138
ID
O4
DT
O1

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Best Local S
Matches 81
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Sclerogiossa; Serpentes; Colubroidea;
Elapidae; Elapinae; Naja.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bambai B., Bredehorst R., Vo
Submitted (MAY-1998) to the
EMBL; AF063190; AAF00693.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-KAOUTHIA; TISSUE-VENOM GLAND;
                                                                                                                                                                                                                             042138 PRELIMINARY; PRT; 620 AA.
042138;
01-JAN 1998 (TrEMBLrel. 05, Created)
01-JAN 1998 (TrEMBLrel. 05, Last sequence update)
01-JUN 2001 (TrEMBLrel. 17, Last annotation update)
METALLOPROTEINASE-DISINTEGRIN-LIKE PROTEIN (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00200; disintegrin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01421; Reprolysin; 1.
                  SEGUENCE FROM N.A. MEDLINE=98052412;
                                                                                                                          Agkistrodon contortrix laticinctus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00050; DISIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001762; Disintegrin. InterPro; IPR002870; Pep_M12B_propep. InterPro; IPR001599; Reprolysin. InterPro; IPR00130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P17494; 1KST
  Selistre De Araujo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPKPNFTDCNRHTQVCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSIRNISQVLEKKRNNCFVES------GQPICGNGMVEQGEECDCGYSDQCKDECCFDA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGNYIMYARATSGDKLNNNKFSL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGIITVQNYGSHVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NATTCKLQHEAQCDSEE----CCEKCKFKGAGAECRAAKDDCDLPELCTGQSAECPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSVREHQRYLLRDRPQCILNKPLSTDIVSPPICGNYFVEVGEECDCGSPADCQSACC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMVAITMAHEMGHNLGMNHDKGF-CTCGFNK-----CVMSTRRTK----PAYQFSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCR-DDSDCAREGICNGFTALCPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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PS50214; DISINTEGRIN_2; 1.
PS00142; ZINC_PROTEASE; UNKNOWN_1.
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  PubMed=9392519;
o H.S., de Souza
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600 Co
67661 MW;
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31.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
COBRIN.
; C7C0D45EBC694290 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 298.5;
Pred. No. 3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
  D.H.,
  Ownby C.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
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time:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50215; ADAM_MEPRO; 1.

PROSITE; PS00427; DISINTEGRIN_1; 1.

PROSITE; PS00147; DISINTEGRIN_2; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

Hydrolase; Protease; Metalloprotease; Zinc; Venom; SEQUENCE 620 AA; 69512 MW; 9016AFEB5AE0BB87 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Analysis of a cDNA sequence encoding a novel member of the snake venom metalloproteinase, disintegrin-like, cysteine-rich (MDC) protein family from Agkistrodon contortrix laticinctus."; Biochim. Biophys. Acta 1342:109-115(1997).

-1- SIMILARITY: CONTAINS A DISINTEGRIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00200; disintegrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002870; Pep_M12B_prop
InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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HSSP; P18619; 1FVL.
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                                                                                                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                                                                                                           177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 KSHDN---AQLLTVIDFDGPTIGKAYMAS-----MCDPKR-----SVGII--Q 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 QNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGIITVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNNNKFSLCSIRNISQVLEKKRNNCFVES-----GQPICGNGMVEQGEECDCGYSDQC 176
689
                                                                                                                                                                                QSAECPTDREQRNGHPCLNDNGYCYN
                                                                                                                                                                                                                                                                                                                              QNPCC-----DAATCKLTPGSQC--ADGVCCD-QCRFTRAGTECRQAKDCDMADLCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHST--INLMMAVTMAHEMGHNLGMDHDE-KYCTCGAKS-----CVMAKALS--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYGSHVPPKVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGNYIMYARATSGDK 123
                                                                                                                                                                                                                                                                                                                                                                                                   KDECCFDANQPEGRKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRD-DSDCAREGICNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPSKLFSNCSQEDYRKYLIKRRPKCILNEPNGTDIVSPPVCGNELLEVGEECDCGSPTNC
                                                                                                                                                                                                                                                         FTALCPASDPKPNFTDCNRHTQVCIN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 29.7 79; Conservative
sec
                              April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pep_M12B_propep.
Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.7%; Score 293; DB 13; 29.7%; Pred. No. 1.3e-19;
                                      2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
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                                                                                                                                                                                                                                                                                                                                      476
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OM protein - protein search, using sw model

Run on: April 1, 2002, 15:12:07; Search time 98
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Run on: April 1, 2002, 15:12:07; Search time 98.78 Seconds
(without alignments)
(109.111 Million cell updates/sec
Title: US-09-871-388-8
Perfect score: 4103
Sequence: 1 MVLPTVLILLSWAAGLGGO......100PPRORPRESYQMGHMRR 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL\_17:\*
1: sp\_archea:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_manumal:\*
7: sp\_mhc:\*
8: sp\_organelle:\*
9: sp\_phage:\*

sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*

sp\_vertebrate:\*
sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 19     | 18                 | 17                 | 16                 | 15                | 14                 | 13                 | 12                 | 11                 | 10                | 9                  | 8                 | 7                 | 6                 | G                  | 4                  | ω                 | N      | <b>-</b>           | Result<br>No.         |
|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------|--------------------|-----------------------|
| 380.5  | 384.5              | 385                | 395.5              | 406               | 409                | 416.5              | 478                | 707                | 1352              | 1397               | 1487.5            | 1489              | 1489.5            | 2956               | 3346               | 3884.5            | 3940.5 | 4103               | Score                 |
| 9.3    | 9.4                | 9.4                | 9.6                | 9.9               | 10.0               | 10.2               | 11.7               | 17.2               | 33.0              | 34.0               | 36.3              | 36.3              | 36.3              | 72.0               | 81.6               | 94.7              | 96.0   | 100.0              | Query<br>Match Length |
| 873    | 604                | 616                | 819                | 75                | 600                | 845                | 686                | 162                | 1537              | 922                | 1236              | 1239              | 1238              | 544                | 691                | 748               | 748    | 749                |                       |
| 13     | 13                 | 13                 | 4                  | σ                 | ü                  | 11                 | տ                  | 13                 | G                 | ري.                | S                 | Ų                 | տ                 | 11                 | 4                  | σ                 | 4      | 11                 | DB                    |
| 042595 | Q9PT48             | Q90495             | Q13443             | 077633            | Q9PVK7             | Q61072             | Q94316             | 042568             | Q9VAI2            | 046354             | Q9NKF9            | Q94902            | 6MLA60            | Q10743             | Q10742             | Q10741            | 014672 | 035598             | ID                    |
|        | Q9pt48 atractaspis | Q90495 echis carin | Q13443 homo sapien | 077633 sus scrofa | Q9pvk7 naja naja ( | Q61072 mus musculu | Q94316 caenorhabdi | 042568 xenopus lae | Q9vai2 drosophila | O46354 caenorhabdi | Q9nkf9 drosophila | Q94902 drosophila | Q9vjw9 drosophila | Q10743 rattus norv | Q10742 homo sapien | Q10741 bos taurus |        | 035598 mus musculu | Description           |

δÃ

1 MVLPTVLILLLSWAAGLGGQYGNPLNKYIRHYEGLSYNVDSLHQKHQRAKRAVSHEDQFL 60

0;

| 45 323             | 44 323.5 |                    |                    | 41 326             |        | 39 329.5           | 38 332.5           | 37 333    | 36 333.5 | 35 337 | 34 337             | 33 337             | 32 337.5 | 31 343.5           |        |        |                    |        | <b>ω</b> | 25 360             | 24 361.5           | 23 365             | 22 372 | 21 375             | 20 377.5           |
|--------------------|----------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|-----------|----------|--------|--------------------|--------------------|----------|--------------------|--------|--------|--------------------|--------|----------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|
| 7.9                | 7.9      | 7.9                | 7.9                | 7.9                | 8.0    | 8.0                | 8.1                | 8.1       | 8.1      | 8.2    | 8.2                | 8.2                | 8.2      | 8.4                | 8.4    | 8.4    | æ<br>.5            | 8.5    | 8.6      |                    |                    | 8.9                |        | 9.1                | 9.2                |
| 739                | 903      | 857                | 549                | 419                | 697    | 829                | 832                | 760       | 610      | 918    | 918                | 760                | 1569     | 609                | 010    | 606    | 505                | 609    | 728      | 617                | 920                | 735                | 620    | 914                | 610                |
| *                  | 11       | 4                  | 13                 | 13                 | 11     | 11                 | 4                  | 11        | 13       | 4      | 4                  | 11                 | υı       | 13                 | 13     | 13     | 3                  | 13     | 4        | 13                 | 11                 | 11                 | 13     | 13                 | 3                  |
| Q9Y3Q7             | Q61824   | Q9UНР2             | Q90500             | Q92043             | Q9R158 | Q9R1V7             | 075077             | Q9R159    | 093523   | Q9BZL5 | Q9Н013             | Q9D4E4             | Q9VFH0   | Q9W6M5             | Q9Y120 | Q98UF9 | 073795             | Q90282 | Q9BZ11   | Q90499             | 035674             | Q60411             | 042138 | 012960             | Q9DGB9             |
| Q9y3q7 homo sapien | 4 mus    | Q9uhp2 homo sapien | Q90500 echis pyram | Q92043 crotalus at | mus    | Q9rlv7 mus musculu | 075077 homo sapien | mus muscu | w        | homo   | Q9h013 homo sapien | Q9d4e4 mus musculu |          | Q9w6m5 agkistrodon |        |        | 073795 agkistrodon |        | 5        | Q90499 echis pyram | O35674 mus musculu | Q60411 cavia porce |        | 012960 xenopus lae | Q9dqb9 crotalus at |

## ALIGNMENTS

| Ma<br>D.Q.  | O35598  ADD DT OO  DT O |
|---|--|
| Query Match<br>Best Local Similarity<br>Matches 749; Conser | 98 98 98 98 98 98 98 735598 101-JAN-1998 (TrEMBLrel 101-JAN-1998 (TrEMBLrel 101-JAN-1998 (TrEMBLrel 101-JUN-2001 (TrEMBLrel 101-JUN-2001 (TrEMBLrel 101-JUN-2001 (TrEMBLrel 101-JUN-2001 (TrEMBLrel 101-JUN-2001 (TrEMBLrel 101-JUN-2001 (TrEMBLrel 10090) 101 101-TaxID-10090; 101 101 101 101 101 101 101 101 101 1   |
| vat   | nontree American School Research   |
| 100.0%; Score 4<br>100.0%; Pred. N<br>Live 0; Misma         | ILINARY; PRT; 749  LICEL. 05, Created)  LICEL. 05, Last sequence  LICEL. 17, Last annotat;  e).  Chordata; Craniata; \(\); Rodentia; Sciurognati  curing Drosophila and during Drosophila and (253303.1;)  dam10.  C53303.1;  disintegrin.  0; Zn_MTpeptdse.  integrin; 1.  rolysin; 1.  rolysin; 1.  SIN; 1.  DISINTEGRIN_2; 0.  ENONEMBERGO; 1.  DISINTEGRIN_2; 0.  ENONEMBERGO; 06CEC3EB20  |
| ore 4103; DB 11;<br>ed. No. 0;<br>Mismatches 0;             | PRT; 749 AA.  **eated)  ist sequence update)  ist annotation update)  Craniata; Vertebrata; Euteleostomi;  Sciurognathi; Muridae; Murinae; Mus  Sciurognathi; Muridae; Murinae; Mus  or processing of Notch and mediates  cophila and vertebrate neurogenesis.  in.  n.  dse.  1. 2; 1. 06CEC3EB32C5F4F94 CRC64;   |
| Length 74<br>Indels   | ta; Euteleostomi;<br>dae; Murinae; Mus<br>tch and mediates<br>ate neurogenesis.  |
| 9;<br>0; Gaps   | tomi;<br>, Mus.<br>ates  |

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SEQUENCE FROM N.A.

MEDLINE-97450992; PubMed-9305925;
Rosendahl M.S., Ko S.C., Long D.L., Breedled, A., Anderson L., Pyle S.M., Morelatyons D., Lichenstein H.S.;

"Identification and characterization of alpha-processing enzyme from the ADAM imetalloproteases.";
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Best Local Similarity
Matches 718; Conserv
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EMBL; AF009615; AACC1766.1; -.

RISSP; P18619; IFVL.

InterPro; IPR001762; Disintegrin.

InterPro; IPR001762; Disintegrin.

InterPro; IPR001300; Reprolysin.

InterPro; IPR001300; Ton_MTpeptdse.

Pfam; PF00200; disintegrin; 1.

Pfam; PF01421; Reprolysin; 1.

PFfam; SM00050; DISIN; 1.

R PROSITE; PS50215; ADAM_MEPRO; 1.

R PROSITE; PS50214; DISINTEGRIN_2; 1.

PROSITE; PS50214; DISINTEGRIN_2; 1.
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Eukaryota; Metazoa; (Mammalia; Eutheria; Fucbl\_TaxID=9606;

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Homo sapiens (Human).
Homo sapiens (Homan).
'~rvota; Metazoa; Chordata; '

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1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ELEVELS IN KLDNEY, SPLEEN, LUNG AND HEART.

1. SIMILARITY: BELLONGS TO PEPTIDASE FAMILY M12C (ZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DISINTEGRIN-METALLOPROTEASE PRECURSOR (EC 3.4.24.-) (MYELIN-ASSOCIATED
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PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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HSSP; P18619; 1FVL.
MEROPS; M12.210; -.
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Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
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-!- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS
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                   DGRFEGFIKTRGGTFYIEPAERYIKDRILPFHSVIYHEDDINYPHKYGPQGGCADHSVFE
                                                           RLDFHAHGRHFNLRMKRDTSLFSEEFRVETSNAVLDYDTSHIYTGHIYGEEGSFSHGSVI
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                                                                                                                                            MVLLRVLILLLSWVAGLGGQYGNPLNKYIRHYEGLSYDVDSLHQKHQRAKRAVSHEDQFL
PF01421; Reprolysin; 1. ; SM00050; DISIN; 1.
                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                   94.78;
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                                                                                                                                                                                                                                                                                                                                   ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                 Score 3884.5;
Pred. No. 0;
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POTENTIAL.
METALLOPROTEINASE
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                      InterPro; PLACE | IPRO01762; Disintegrin.
InterPro; IPRO01590; Reprolysin.
InterPro; IPRO01390; Zn_MTpeptdse.
Pfam; PPO0200; disintegrin; 1.
Pfam; PPO0421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
                                                                                                                                                                                                                                                                                                                              Q10742 PRELIMINARY;
Q10742; Q92650;
Q107042; Q92650;
Q1.00V-1996 (TIEMBLTel. 01, C
Q1.JAN-1998 (TIEMBLTel. 05, L
Q1.JUN-2001 (TIEMBLTel. 17, L
DISINTEGRIN-METALLOPROTEASE M
           PRINTS; PRO0289; DISIN; SMART; SM00050; DISIN;
                                                                                                                                  disintegrin-metalloprotease expressed Biochem. J. 317:45-50(1996).
EMBL; Z48579; CAR68463.1; -.
HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                         MEDLINE=96276398; PubMed=8694785;
Howard L., Lu X., Mitchell S., Griffths S., Glynn P.;
"Molecular cloning of MADM: a catalytically active mammalian"
                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
PROSITE;
                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=96276398;
                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                    MEROPS; M12.210;
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 PS50215;
ADAM_MEPRO;
                                                                                                                                                                                                                                                                                     Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                               Last sequence update)
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MADM (FRAGMENT).
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Best Local Similarity
Matches 612; Conser
                                                   Q10743 PRELIMINARY; PRT; 544
Q10743;
Q10743;
Q10743;
Q10743;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation of the control o
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                Ratțus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
   NCBI_TaxID=10116;
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ilarity 88.4%;
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ZINC_PROTEASE;
                Chordata;
Rodentia;
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77632
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PRECURSOR (EC 3
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Pred.
                Craniata; Vertebrata; Sciurognathi; Muridae.
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No. 4
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3.4.24.-)
                  Muridae;
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                                                                          (MYELIN-ASSOCIATED
                   Murinae;
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Matches
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InterPro; IPR001500; Reprolysin
InterPro; IPR001300; Zn_MTpeptol
Pfam; Pr00200; disintegrin; 1.
Pfam; Pr01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
SMART; SM00050; DISIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
ACT_SITE
METAL
METAL
METAL
CARBOHYD
CARBOHYD
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SEQUENCE
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Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;
Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;
Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;
Howard L., Mitchell S., Lu X., Griffiths S., Glynn P.;

"Molecular cloning of MADM: a catalytically active mammalian disintegrin-metalloprotease expressed in various cell types."

Blochem. J. 317:45-50(1996).

-1- SUBCELTULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SUBCELTULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SUBCLARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC METALOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBBRAMILY.
-1- SIMILARITY: HIGH, IN THE MIDDLE REGION, TO DISINTEGRINS.
BSSP; D18619; IFVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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PROSITE; PS50214; DISLIVEGERIN_2; 1.
PROSITE; PS501142; ZINC_PROTEASE; UNKNOWN_1.
Integrin; Hydrolase; Metalloprotease; Trans;
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SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
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                                                                                                                DGVLGLAWVGAPSGSSGGICEKSKLYSDGKKKSLNTGIITVQNYGSHVPPKVSHITFAHE
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PSQGPCCTAQCAFKSKSEKCRDDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVCIN
             PSQGPCCTAQCAFKSKSEKCRDDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVCIN
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98.5%;
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Reprolysin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MW.
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BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

N-LINKED (GLONAC. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).
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DISINTEGRIN.
EXTRACELLULAR (POTI
POTENTIAL.
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Pred. No. 1.9e
4; Mismatches
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No. 1
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RA Abrill J.F., Agbayani A. An H.J. Andrews-Pfannkoch C.R., Malson C.R., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bandari D., Bolshakov S., Ra Beeson K.Y., Benos P.V., Berman B.P., Bandari D., Bolshakov S., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Rotler R., Chandra I., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dodoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Allaris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Spiere E., Spradling A.C., Stapleton M., Strong R., Sun E., Shen H., Ra Ra Sylere E., Spradling A.C., Stapleton M., Strong R., Sun E., Shen H., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M. Weissenbach J., Ra Alesson D.R., Woodseye T., Worley K.C., Wu D., Yang S., Yao Q.A., Ra Alesson S.A., Myers E.M., Rubin G.M., Venter J.C., Sheng L., Ra Zheng X.H., Zhong F.N., Zhong W., Zhon W., Shu S., Zhu X., Smith H.O., Ra Zheng X.H., Zhong F.N., Zhong W., Zhon W., Shu S., Zhu X., Smith H.O., Ra Zheng X.H., Zhong F.N., Zhong W., Zhon W., Shu S., Zhu X., Smith H.O., Ra Zheng X.H., Zhong F.N., Zhong W., Zhon X., Zhu X., Smith H.O., Scheeler E., Spradle D., Ra Zhong M., Shu S., Zhu X., Smith H.O., Ra Zheng X., La Shu S., Zhu X., 
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01-MAY-2000
01-MAY-2000
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PROSITE; PS50215; ADAM_MEPRO; 1.

PROSITE; PS50214; DISINTEGRIN_2; 1.

PROSITE; PS50214; ZINC_PROTEASE; UNKNOWN_1.

PROSITE; PS50142; ZINC_PROTEASE; UNKNOWN_1.

PROSITE; PS60142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003640; AAF53318.1;
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TALCIRGECSGSPCLLWNMTKCFLTSTTLPHVSKRKLCDLACQDGNDTSTCRSTSEFADK
                                  TQVCINGQCAGSICEKYDLEEC--TCASSDGKDNKELCHVCCMKKMAPSTCASTGSLQWS
                                                                                                                                                                                                                                                                                                                   GICEKSKLYSD-----GKKKSLNTGIITVQNYGSHVPPKVSHITFAHEVGHNFGSPHD
                                                                                                                                                                                                                                                                                                                                                                                         DEKDPTNPFRFPNIGVEKFLELNSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIY---HEDDINYPHKYGPQGGCA----
                                                                                                     QCSPSQGPCCTA-QCAF--KSKSEKCRDDSDCAKEGICNGFTALCPASDPKPNFTDCNRH
                                                                                                                                                                                 CFVESGQPICGNGMVEQGEECDCGYS-DQCKDDCCF----DANQPEGKKCKLKPGK
                                                                                                                                                                                                                                                          SGTECTPGESKNLGQKENGNYIMYARATSGDKLNNNKFSLCSIRNISQVLE----KKRNN
                                                                                                                                                                                                                                                                                              GICEKYKTYTETVGGQYQSTKRSLNTGIITFVNYNSRVPPKVSQLTLAHEIGHNFGSPHD
                                                                                                                                                                                                                                                                                                                                                                                                                                             GRKYEVDEKTREEITSLIAHHVTAVNYIYRNTKFDGRTEHRNIRFEVQRIKIDDDSACRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHQLVHERVRRATDNGAGDRGSSGGSGRGREDNKNTCSLYIQTDPLIWRHIREGIADHDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKKSAPQQQQQPHPPKKYISGDEDFKYPHQKYTKEANFAEGAFYDPSTGRRLGSSANVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAHGRQFNLRMKRDTSLFSDEFKVETSNKVLDYDTSHIYTGHIYGEEGSFSHGSVIDGRF
                                                                       QCSPSQGPCCLSNSCTFVPTSYHQKCKEETECSWSSTCNGTTAECPEPRHRDDKTMCNNG
                                                                                                                                              CFKASEGAFCGNKIVESGEECDCGFNEEECKDKCCYPRLISEYDQSLNSSAKGCTRRAKT
                                                                                                                                                                                                                       YPQECRPGGL-----NGNYIMFASATSGDRPNNSKFSPCSIRNISNVLDVLVGNTKRD
                                                                                                                                                                                                                                                                                                                                                                     SYNGPHNAFCNEHMDYSNFLNLHSLEDHSDFCLAYVFTYRDFTGGTLGLAWVASASGASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQMTGVEEGARAHPEKHAASSG-----PELLRKKRTTLAE---------
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337; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GTREAVIAQISSHVKAIDTIYQTTDFSG---IRNISFMVKRIRINTTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1489.5; DB 5;
Pred. No. 1.7e-112;
Il; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RNTCOLYIOTDHLFFKYY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
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848
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184

153 195

255

75

22;

451 615 395

495

282

| Query Match  36.3%; Score 1489; DB 5; Length 1239;  Best Local Similarity 34.4%; Pred. No. 1.9e-112;  Matches 337; Conservative 131; Mismatches 267; Indels 246; Gaps 22;  Qy 7 LILLLSWAAGLGG-QYGNP-LNKYIRHYEGLSYNVDSLHQKHQRAKRAVSHEDQFLLLDF 64;  | SULT 7 4902 Q94902 Q949 | Oy 618 KQFSGTTITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKKAIFSPQLYENIAEWIVA 677  Db 849 YNIQKGGISLQPGSPCNNFQGYCDVFLKCRAVDADGPLLRLKNLLLNRKTLQTVAEWIVD 908  Qy 678 HWMAVLLMGIALINLMAGFIKICSVHTPSSNPKLPPKPLPGTLKRRPPOPIQ 731  LI:  :   :    : |
|---|--|--|
| RESULT 8  Q9NKF9 ID Q9NKF9; AC Q9NKF9; AC Q9NKF9; DT 01-OCT-2000 (TrEMBLrel. 15, Created) DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-OCT-2000 (TrEMBLrel. 17, Last annotation update) DE KUZ PROTEIN. GN KUZ OR BG:DSS7660.3 OR CG7147. OS Drosophila melanogaster (Fruit fly). OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; CC Eptygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila. OC MCBL_TaxID=7227; RN [1] RP SEQUENCE FROM N.A. STRAIN=Y, CN BW SP; RX MEDLINE=99403001; PubMed=10471707; RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., RA Celniker S., Rubin G.M.; Spradling A., Tsang G., Wan K., Whitelaw K., RA Celniker S., Rubin G.M.; | Qy 283 -DEKDPTNPERFRPNIGVEKTELLINSEQNHDDYCLAVPTDRDEDGVCLALAWGASGAS 495 Qy 283 -DEKDPTNPERFRPNIGVEKTELLINSEQNHDDYCLAVPTDRDEDGVCLALAWGASGAS 341 H  | OY 184 KYOMTGVEEGARAHPEKHAASSGPELLRKKRTTLAE  |

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Best Local
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InterPro; IPR001762; DlSintegrin.
InterPro; IPR001762; DlSintegrin.
InterPro; IPR00130; Zn MTpeptdse.
SMART; SM0050; DISIN; 1
PROSITE: PS0015; ADAM_MEPRO; 1
PROSITE: PS50215; ADAM_MEPRO; 1
PROSITE: PS50214; DISINTEGRIN_2; 1.
PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1236 AA; 136343 MW; 40461AC17040C9AD (
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AE003407; AAF44800.1; -.
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   627
                                                     416 YIMYARATSGDKLNNNKFSLCSIRNISQVLE----KKRNNCFVESGQPICGNGMVEQGEE
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KKSLNTGIITVQNYGSHVPPKVSHITFAHEVGHNFGSPHDSGTECTPGESKNLGQKENGN 415
                                                                                                                                                                                                                                          NLHSLEDHSDFCLAYVFTYRDFTGGTLGLAWVASASGASGGICEKYKTYTETVGGQYQST
                                                                                                                                                                                                                                                                                                   ELNSEQNHDDYCLAYVFTDRDFDDGVLGLAWVGAPSGSSGGICEKSKLYSD-----GK
                                                                                                                                                                                                                                                                                                                                                                HVTAVNYIYRNTKFDGRTEHRNIRFEVQRIKIDDDSACRNSYNGPHNAFCNEHMDVSNFL
                                                                                                                                                                                                                                                                                                                                                                                                                      HVKAIDTIYQTTDFSG----IRNISFMVKRIRINTTS----DEKDPTNPFRFPNIGVEKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSSGGSGRGREDNKNTCSLYIQTDPLIWRHIREGIADHDRGRKYEVDEKTREEITSLIAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDEDFKYPHQKYTKEANFAEGAFYDPSTGRRLGSSANVADWHQLVHERVRRATDNGAGDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RNTCQLYIQTDHLFFKYY-----
                                                                                                                     KRSLNTGIITFVNYNSRVPPKVSQLTLAHEIGHNFGSPHDYPQECRPGGL-----NGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DHSVFERMRKYQMTGVEEGARAHPEKHAAS
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                                                                                                                                            Query Match
Best Local S
Matches 314
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01-JUN-1998
01-JUN-2001
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046354;
                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wen C., Metzstein M.M., Greenwald I.; "SUP-17, a Caenorhabditis elegans ADAM protein related KUZBANIAN, and its role in LIM-12/NOTCH signalling."; Development 124:4759-4767(1997).
                                                                                                                                                                                                                                                                                                                                             EMBL; Z96047; CAB09416.1; - HSSP; P18619; 1FVL.
                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF024614; AAB97161.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98088688; PubMed*9428412;
Wen C., Metzstein M.M., Greenwald
"SUP-17, a Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
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                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                         SMART; SM00050; DISIN;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                     InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                MEROPS; M12.210;
                                                                                                                                                                                                                                                                                                                InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                      ennard N.
  137
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                                                                                                                                            Local Similarity es 314; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKSEKCRDDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVCINGQCAGSICEKYDLE
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                                              DTSLFSDEFKVETSNKVLDYDTSH-IYTGHIYGEEGSFSHGSVIDGRFEGFIKTRGGTFY
                                                                                                               NPLNKYIRHYEGLSYNVDSLHQKHQRAKR----AVSHEDQFLLLDFHAHGRQFNLRMKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCCAVHTPSSNPKKRRARRISETLRAPMNTLRRMQRHPNQRGAGPRSIPPPAHEAQHYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KICSVHTPSSNPKLPPPKPLPGTLK-----RRRPPQPIQQ--PPRQRPRESYQMGHMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYCDVFLKCRAVDADGPLLRLKNLLLNRKTLQTVAEWIVDNWYLVVLMGVAFIVVMGSFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYHQKCKEETECSWSSTCNGTTAECPEPRHRDDKTMCNNGTALCIRGECSGSPCLLWNMT
                             DDSLFHEDHMSDVDGGYADIKPSHFLYEGYLKDDPNSHVHGSVFDGVFEGHIQTGEGRRY
                                                                                    NGLNNFIDNFETLNYRATHVANQVTRRKRSIDSAASHYQEPIGFRFNAYNRTFHVQLHPI 84
                                                                                                                                                                                                             PS50215; ADAM_MEPRO; 1.
PS50214; DISINFEGRIN.2; 1.
PS00142; ZINC_PROTEASE; UNKNOWN.1
PS02 AA; 101572 MW; BAE4E5E658
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3 (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                             Conservative
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37.6%; Po
ative 132;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last
                                                                                                                                            Score 1397; DB 5;
Pred. No. 3.9e-105;
2; Mismatches 246;
                                                                                                                                                                                                                  BAE4E5E65875CDB1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                      Length 922;
                                                                                                                                             Indels 142;
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| Db 202 -EMTDVQNISGESTDFFTNYMTMGG  258 IRMKEGNNDPIRTREEIVSLEYNH  258 IRMKEGNNDPIRTREEIVSLEYNH  258 IRMKEGNNDPIRTREEIVSLEYNH  258 IRMKEGNNDPIRTREEIVSLEYNH  259 340 SSGGICEKSKLYSDGKKKSL  259 340 SSGGICEKSKLYSDGKKKSL  261 11   | Db  |
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| YQWTGVEEGARAHP :         :        :  | 145 |
| DHLIFFKY      ::: DHKLYEH  TTSD     (ap)   (ap) |     |

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RA Beceson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Borkstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Meirkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentalov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menta S.M., Moyd M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Sangders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Ra Harisas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Zhon M., Zhong K., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhon M., Zhang G., Zhao Q., Zheng L.,
Spitch S., Spitch B., Shill M., Shill M.C., Smith H.O.,
C. Dinkin R., Shill M., Shill M., Shill M.S., Zhu X., Smith H.O.,
RA Cibbs R.A., Mersens H., Shi
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01421; Reprolysin; 1.

SMART; SM0050; DISIN; 1.

PROSITE; PS50214; DISINTEGRIN_2; 1.

PROSITE; PS50214; DISINTEGRIN_2; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase; Metalloprotease; Zinc.
SEQUENCE 1537 AA; 168796 MW; 46A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0039688; CG1964.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
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    187
                                                249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VLILLLSWAAG-------LGGQYGNPLNKYIRHYEGLSYN-------VDSLHQKHQ 47
                                                                                                                                                                                                                                                             YTGHIYGEEGSFSHGSVI---DGRFEGFIKTRGGTFYIEPAERYIKDRI-LPFHSVIYHE 158
                                                EVPYNDDFRVLASEEDKSEESPRKYPTTSTTRSTVRSTESFLATLTKPTSNRNILVNNYN 308
                                                                                                                                        SDVNMQKQQFTGGGLNSATPAKTHCASEKLRKKRWLPEELAMSDAPAPTYNRNPPLPLDL 248
                                                                                                                                                                                      DDINYPHKYGPQGG-----CADHSVFERMRK---------
                                                                                                                                                                                                                                  YTGSL--EDDEAAHVQAILTSDNLLDGTIETQAEHYYIEPAHRYSQQLAESGVHSIVYKL 188
                                                                                                                                                                                                                                                                                                                               RQKREVTPSASGLAHTIRLNFSAHDRDFRLVLRQQPHSVFAHDVEIENTLGPIDYDVSRI 130
                                                                                                                                                                                                                                                                                                                                                                        RAKRAVSHEDQFLL----LDFHAHGRQFNLRMKRDT-SLFSDEFKVETSNKVLDYDTSHI 102
                                                                                                                                                                                                                                                                                                                                                                                                                         VLFLWLLWLPGEILAIPTPLKLPG-YTHRLTPYIKHWEAANFDRQVLQAAQVRHLEQARF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metalloprotease;
1537 AA; 168796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 112;
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32.8%;
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168796 MW; 46A52344A8E73617 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1352; DB 5;
Pred. No. 3.6e-101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1537;
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042568;
01-JAN-1998
01-JAN-1998
01-JUN-2001
                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                         lateral inhibition during Drosophila (el1 90:271-280(1997), EMBL, AFO11380; ARC60248.1; -. HSSP, P18619; 1FVL.
                                                                                                    SEQUENCE FROM N.A. MEDLINE-97386452; PubMed-9244301;
                                                                                                                                                                                                                              KUZBANIAN (FRAGMENT).
  InterPro;
               MEROPS; M12.210;
                                                                                            Pan D.,
                                                                                                                                                NCBI_TaxID=8355;
                                                                           Kuzbanian controls proteolytic processing of Notch and mediates
                                                                                                                                                                                                                                                                                                                                                                  947
                                                                                                                                                                                                                                                                                                                                                                                                                      887
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                                                                                                                                                                                                                                                                                                                                                                                                                                NDFRGYCDVFMRCRLVDADGPLARLKKAIFSPQLYENIAEWIVAHWWAVLLMGIALIMLM
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                                                                                                                                                                                                                                                                                                                                                                                          AGFIKICSVHTPSSNPKL 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYDLEECTCASSDGKDNKELCHVCCMKKMAPSTCASTGSLQWSK-QFSGRTITLQPGSPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSICGNGVVEPGEQCDCGWEEDCKDSCCFPMSRQPRLDETPCTLTPHARCSPSQGPCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPGESKNLGQKENGNYIMYARATSGDKLNNNKFSLCSIRNISQVLEKKRNN----CFVESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGVCEKNGHYR-GSLKSLNTGIVTLLNYGKHVPPAVSHVTLAHEIGHNFGSPHDP-EQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMKDPS--YRFPGNYGVEKFLELFSEEDYDAFCLAYMFTYRDFEMGTLGLAWTG-DLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYLQADHTFFQKMGSDEASIEAITRHYQRANTIYRNTDFNNDGKPDNITFMIKRIKVHNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYIQTDHLFFKYYGTREAVIAQISSHVKAIDTIYQTTDFSG---IRNISFMVKRIRINTT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIIVNNYNPEIIFAPNPHNPSFNSMMMTNLLSGRGGEDIHSSPRLLYDRKT----TCM
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                                                                                            Rubin G.M.;
IPR001762; Disintegrin
                                                                                                                                                                                                                                        B (TrEMBLrel.
B (TrEMBLrel.
l (TrEMBLrel.
                                                                                                                                                                                                                                                                                               PRELIMINARY;
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05,
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Last sequence update)
Last annotation updat
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Best Local
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   PROSITE;
                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q94316, PRELIMINARY;
Q94316, Q194316, Q2,
Q1-FEB-1997 (TrEMBLrel. Q2,
Q1-FEB-1997 (TrEMBLrel. Q2,
Q1-JUN-2001 (TrEMBLrel. 17,
                               SMART; SM00050; DISIN;
                                         InterPro; IPR001590; Reprolysin.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                        EMBL; U70844; AAB09097.1;
HSSP; P17494; 1KST.
                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1997 (TYEMBLEe). 02, Last sequence update)
01-UN-2001 (TYEMBLEE). 17, Last annotation update)
SIMILARITY TO METALLOPROTEASES.
                                                                        InterPro; IPR001762; Disintegrin.
                                                                                                                        Submitted (SEP-1996)
                                                                                                                                        Waterston R.;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50214; DISINTEGRIN_2;
NON_TER 1 1 1 1
NON_TER 162 162
SEQUENCE 162 AA; 17780 MW; E:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00289; DISINTEGRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSDOCKDDCCFDANQPEGKKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKCRDDSDCAKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVCCMEKMIPHTCASTGSEVWKAYFKGKTITLQPGSPCNEFK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVCCMKKMAPSTCASTGSLQWSKQFSGRTITLQPGSPCNDFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICNGFTALCPASDPKPNFTDCNRHTQVCINGQCAGSICEKYDLEECTCASSDGKDNKELC 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSDQCKDECCYDANQPENLKCTLKPGKQCSPSQGPCCTTGCTFKRAGENCREESDCAKMG
PS50214; DISINTEGRIN_2;
               PS50215;
                                                                                                                                                                                               (OCT-1996) to
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               ADAM_MEPRO;
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17780 MW;
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72.2%;
                                                                                                                      to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
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PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.

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SEQUENCE
                                   Q61072 PRELIMINARY; PRT; 845 AA. Q61072; Q60618; Q61853; Q1954; Q61853; Q1-JUL-1997 (TrEMBLrel. 04, Created) 01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat CELLULAR DISINTEERIN-RELATED PROTEIN PRECURSOR (MADAM9 OR MLTNG OR MDC9.
Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                              582
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S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDTIY-----QTTDFSG---IRNISFMVKRIRINTTSDEKDPTNPFRFPNI-GVEKF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SYPHQLSDDLGPVVGYFESDLDLNLDLSAMPVRNQVSFRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIKDRILPFHSVIYHEDDINYPHK----YGPQGGC--ADHSVFERMRKYQMTGVEEGARA 196
                                                                                                                                                                                                                                                                                                VFMRCRLVDADGPLARLKKAI------FSPQLYENIAEWIVAHWWAVLLMGIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEQGEECDCGYSDQCKDDCCFDANQPEGKKCKLKPGKQCSPSQGPCCTAQCAFKSKSEKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLNTGIIT -- VQNYGSHVP--PKVSHITFAHEVGHNFGSPHD-----SGTECTPGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LREFAFAEGSKDFCLVHLVTARTFREVATLGLAYVSYKKWDETAGGICSKQETF-NGRVA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-ELNSEQNHDDYCLAYVFTDRDFDD-GVLGLAWVGAP--SGSSGGICEKSKLYSDGKKK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPFLKHRRAIAIPSDRRKDVLNVKRNRCTLKLVADYSFYSIFGKNNTGIVTKFLVNMIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HP-EKHAASSGPELLRKKRTTLAERNTCQLYIQTDHLFFKYYGTREAVIAQ--ISSHVKA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMLMAGFIKI
                                                                                                                                                                                                                                                                                                                                                              TCASSDGKDNKELCHVCCMKKMAPSTCASTGSLQWSKQFSGRTITLQPGSPCNDFRGYCD
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                                                                                                                                                                                                                                                                                                                                                                                                                      -- RDDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQVCINGQCAGSICEKYDL--EEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEDGEECDNGVDTDNEFNCC-----DKFCRLAVGAKCSPLNHICCTPTCQFHNSTHVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----QNGGKYLMSQYAQKGYDANNVLFSPCSRKLIRDVLIGKWESCFQEEMTSFCGNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNLGOKENGNY IMYARATSGDKLNNNKFSLCSIRNISQVLEKKRNNCFVESGQPICGNGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNEIYTPINWDVGKEDDISGRGRFQNMGFSIKEIKVLDRPNASD-SHYNSYSRIWEVERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KVLDYDTSHIYTGHIYGEEGSFSHGSVIDGRFEGFIKTRGGTFYIEPAER 142
                                                                                                                                                                                                                                                                                                                                IC----
                                                                                                                                                                                                                                                                     -----RDRKCVNEVVDNVRNYFLITFQTTGGVLEFIKTH--IVVIAIIFF
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180; Conserv
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       Chordata;
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24.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66D58008A207AE49 CRC64;
       Craniata;
         Vertebrata;
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                                                                  update)
                                                    (MELTRIN GAMMA).
                                                                                                                                                                                                                                                                                                                                HVYLRDGVRCS - - KGSC -
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"A family of cellular proteins related to snake venom disintegri
"A family of cellular proteins related to snake venom disintegri
Proc. Natl. Acad. Sci. U.S.A. 91:2748-2751(1994).

-I. FUNCTION: MAY MEDIATE CELL-CELL OR CELL-MATRIX INTERACTIONS.
-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I. TISSUE SPECIFICITY: WIDELY EXPRESSED.
-I. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-I. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-I. SIMILARITY: BAA18424.1;
-I. SIMILARITY: BAA18424.
                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50215; ADAM_MEPRO; 1.

PROSITE; PS50214; DISINTEGRIN_2; 1.

PROSITE; PS01186; EGE 2; UNKNOWN_1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

Signal; Glycoprotein; Transmembrane; EGF-like domain; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
SMART; SM00181; EGF; 1.
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HSSP; P18619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 426-575 FROM N.A. MEDLINE=96026308; PubMed*7566181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96178079; PubMed=8647900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature
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SEQUENCE
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                              Metal-binding.
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irPro; IPR001762; Disintegrin.

irPro; IPR000561; EGF-11ke.

irPro; IPR002870; Pep_M12B_propep.

irPro; IPR001590; Reprolysin.

irPro; IPR000130; Zn_MTpeptdse.
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ZINC (CATALYTI
                                                                                            N-LINKED
 N-LINKED (GLCNAC. . .) (P
17562E89D4A61674 CRC64;
                                                                                                                                                                                         ZINC
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                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CELLULAR DISINTEGRIN-RELATED
                                                         N-LINKED
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(CATALYTIC) (BY SIMILARITY)
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               D (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                     SIMILARITY)
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Query Match

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           SEQUENCE FROM N.A.

STRAIN-KAOUTHIA; TISSUE-VENOM GLAND;
STRAIN-KAOUTHIA; TISSUE-VENOM GLAND;
SHADAI B., Bredehorst R., Vogel C.-W.;
Bambai B., Bredehorst R., Vogel C.-W.;
Submitted (WAY-1998) to the EMBL/GenBank/DDBJ date
EMBL; AF063190; AAF00693.1; -
HSSP; P17494; IKST.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001190; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                          OSPVK7; PRELIMINARY;
OSPVK7;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
COBRIN PRECURSOR.
                                                                                                                                                                                                       Naja naja (Indian cobra).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Elapinae; Naja.
                                                                                                                                                                                               NCBI_TaxID=35670;
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        PF00200;
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                       077633 PRELIMINARY; PRT; 75 AA. 077633; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) DISINTEGRIN-METALLOPROTEINASE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
SIGNAL
ADAM-10.
Sus scrofa (Pig).
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Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDdm; PD000664; Disintegrin; 1.
SMART; SM00059; DISIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50215; ADAM_MEDRO; 1.
PROSITE; PS50214; DISINTEGRIN_2;
PROSITE; PS00142; ZINC_PROTEASE;
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                                                                                                                                                                                                                                                       CYNGKCPIMTNQCIALRGPGVKVSRDSCFTLNQRTRGCGLCRMEYGRKIPCAAKDVKCGR
                                                                                                                                                                                                                                                                                     CINGQC----
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                                                                                                                                                                                                                                                                                                                                                                                                                  NCFVES-----GQPICGNGMVEQGEECDCGYSDQCKDDCCFDANQPEGKKCKLKPGKQ
                                                                                                                                                                                                                                                                                                                                                      CSPSQGPCCTAQCAFKSKSEKCR-DDSDCAKEGICNGFTALCPASDPKPNFTDCNRHTQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPHDSGTECTPGESKNLGQKENGNYIMYARATSGDKLNNNKFSLCSIRNISQVLEKKRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRAKRAVSHEDQF1LLDFHAHGRQFNLRMKRDTSLFSDEF------KVETSNKVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMNHDKGF-CTCGFNK-----CVMSTRRTK----PAYQFSSCSVREHQRYLLRDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWSNINEINVQSDVKATLDLF-----GEWREKKLLPRKRNDN----AQLLTGIDFNGTPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I-----RINTTSDEKDPTNPFRFPNIGVEKFLELNSEQNHDDYCLAYVFTDRDFDDGVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAEK-YIEFYMVVDNIMYRHYKRNQLVIKRKVYEMINTMNMIYRRLNF----HIALIGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAERNTCQLYIQTDHLFFKYYGTREAVI-AQISSHVKAIDTIYQTTDFSGIRNISFMVKR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H---CYYHGYFQNEADSSAVISACDG-LKGHFKLQGEIYFIEPLK--ISDS--EAHA-IY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QNPQPETKYEDT-MQYEFQVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAYIGS-----TCNP------KTSAAVVQDYSKST--RMVAITMAHEMGHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDENVEEEDETPKICGVTD-TTWESDEPIKKTSL-------LTNTPE----QDRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEDDINYPHKYGPQGGCADHSVFERMRKYQMTGVEEGARAHPEKHAASSGPELLRKKRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDTSHIYTGHIYGEEGSFSHGSVIDGRFEGFIKTRGGTFYIEPAERYIKDRILPFHSVIY
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Pred. No. 6.8e-25
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244

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216

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SEQUENCE
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SEQUENCE FROM N.A.

Flannery C.R., Little C.B., Caterson B., Hughes C.E.;

"Expression of articular cartilage metalloproteinases by chondrocytes
in fresh tissue and explant, monolayer and agarose cultures.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF069645; AAC3529:1; -.

MEROPS; M12.210; -.

MEROPS; M12.210; -.

InterPro; IPR001590; Reprolysin.

PROSITE: PS50215; ADAM_MEPRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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                                                                                                                                       453 FVESGQPICGNGMVE 467
                                                                               61 FVESGOPICGNGMVE 75
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75 75
75 AA; 8224 MW; C03B70C901333557 CRC64;
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